

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: October 13, 2006, 16:14:09 ; Search time 686 Seconds  
(without alignments)  
10776.605 Million cell updates/sec

Title: US-10-623-155-160

Perfect score: 3951

Sequence: 1 tctgcatccattgaaac.....taattaaaacataaaaaa 3951

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:\*

- 1: /EMC\_Celerra\_SID33/ptodata/2/ina/1 COMB.seq:\*
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- 3: /EMC\_Celerra\_SID33/ptodata/2/ina/6A COMB.seq:\*
- 4: /EMC\_Celerra\_SID33/ptodata/2/ina/6B COMB.seq:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3951	100.0	3951	US-09-643-597-160	Sequence 160, App
2	3951	100.0	3951	US-09-480-884A-160	Sequence 160, App
3	3951	100.0	3951	US-09-542-615A-160	Sequence 160, App
4	3951	100.0	3951	US-09-606-421B-160	Sequence 160, App
5	3951	100.0	3951	US-09-221-107-160	Sequence 160, App
6	3951	100.0	3951	US-09-466-396A-160	Sequence 160, App
7	3951	100.0	3951	US-09-476-496A-160	Sequence 160, App
8	3951	100.0	3951	US-09-630-940B-160	Sequence 160, App
9	3951	100.0	3951	US-09-285-479-160	Sequence 160, App
10	3951	100.0	3951	US-10-007-700-160	Sequence 160, App
11	3616.4	91.5	3669	US-09-949-016-2224	Sequence 2224, App
12	3104.4	78.6	3156	US-09-519-172-86	Sequence 86, Appl
13	3101.2	78.5	3190	US-09-623-624-3	Sequence 3, Appl
14	3101.2	78.5	3190	US-10-270-595-3	Sequence 3, Appl
15	2930	74.2	2970	US-09-193-562D-31	Sequence 31, Appl
16	2930	74.2	2970	US-10-055-412B-31	Sequence 31, Appl
17	2800.8	70.9	3362	US-09-643-597-167	Sequence 167, App
18	2800.8	70.9	3362	US-09-480-884A-167	Sequence 167, App
19	2800.8	70.9	3362	US-09-542-615A-167	Sequence 167, App
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21	2800.8	70.9	3362	US-09-466-396A-167	Sequence 167, App
22	2800.8	70.9	3362	US-09-476-496A-167	Sequence 167, App
23	2800.8	70.9	3362	US-09-630-940B-167	Sequence 167, App

24	2800.8	70.9	3362	3	US-09-285-479-167	Sequence 167, App
25	2800.8	70.9	3362	3	US-10-007-700-167	Sequence 167, App
26	2772	70.2	2784	3	US-09-643-597-168	Sequence 168, App
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32	2772	70.2	2784	3	US-09-630-940B-168	Sequence 168, App
33	2772	70.2	2784	3	US-09-285-479-168	Sequence 168, App
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35	2742.6	69.4	8031	3	US-09-643-597-254	Sequence 254, App
36	2742.6	69.4	8031	3	US-09-480-884A-254	Sequence 254, App
37	2742.6	69.4	8031	3	US-09-542-615A-254	Sequence 254, App
38	2742.6	69.4	8031	3	US-09-606-421B-254	Sequence 254, App
39	2742.6	69.4	8031	3	US-09-476-496A-254	Sequence 254, App
40	2742.6	69.4	8031	3	US-09-630-940B-254	Sequence 254, App
41	2740.2	69.4	8031	3	US-10-007-700-254	Sequence 254, App
42	2740.2	69.4	8031	3	US-09-643-597-358	Sequence 358, App
43	2740.2	69.4	2773	3	US-09-630-940B-358	Sequence 358, App
44	2740.2	69.4	2773	3	US-10-007-700-358	Sequence 358, App
45	2619	66.3	2646	3	US-10-007-700-431	Sequence 431, App

#### ALIGNMENTS

##### RESULT 1

US-09-643-597-160  
; Sequence 160, Application US/09643597  
; Patent No. 6426072  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Fan, Liqun  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Hosken, Nancy  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: McNeill, Patricia D.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.455C11  
; CURRENT FILING DATE: 2000-08-21  
; CURRENT APPLICATION NUMBER: US/09/643,597  
; NUMBER OF SEQ ID NOS: 369  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 160  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-643-597-160

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Best Local Similarity	100.0%;	Pred. NO. 0;		
Matches 3951;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;
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DB	1	TCTGATCCATATTGAAACCTGACACATGTATGCGAGGCTCAGTGTGAGTGAAGCTG	60	
QY	61	GAGGCTTCTCTCAACATGACCAAGGAGCATTCGAGGTCTCTATTGCAACTGAAGTT	120	
DB	61	GAGGCTTCTCTCAACATGACCAAGGAGCATTCGAGGTCTCTATTGCAACTGAAGTT	120	
QY	121	TGTGACTCTCTGGTTCCTTAAGTTTCAAGTTCAGAACTCCCATTCCTGGGAGCTGGAGTACAGCT	180	
DB	121	TGTGACTCTCTGGTTCCTTAAGTTTCAAGTTCAGAACTCCCATTCCTGGGAGCTGGAGTACAGCT	180	
QY	181	TCAGACATGGGTATATGATGCTCATTCGAATTAATCTCAGGTACCTGAGATCA	240	

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 13, 2006, 18:05:02 : Search time 471 Seconds

(without alignments)  
6642.696 Million cell updates/sec

Title: US-10-623-155-161

Perfect score: 4942

Sequence: 1 MTQSIAGPICNLKVTLLV.....HHTLSKKRADKNGTKLL 943

Scoring table:

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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
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Searched: 3380774 seqs, 1105942010 residues

Total number of hits satisfying chosen parameters: 6761548

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Pending\_Patents\_NA\_New -QFMT=fastap -SUFFIX=p2n.rnnp -MINMATCH=0.1  
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	4939	99.9	2832	8	US-11-371-354-64288
3	4939	99.9	3669	6	US-10-533-069-578
4	4939	99.9	3955	1	PCT-US06-33148-1637
5	4939	99.9	3955	8	US-11-431-708-4126
6	4939	99.9	3955	8	US-11-475-062-7433
7	4939	99.9	4007	1	PCT-US06-33148-21
8	4939	99.9	4007	8	US-11-363-151-13

9	4939	99.9	4022	1	PCT-US06-33148-1639
10	1996	40.4	3350	8	US-11-475-062-9462
11	1993	40.3	3311	1	PCT-US06-33148-23
12	1993	40.3	3311	8	US-11-475-062-9463
13	1993	40.3	3311	9	US-60-836-986-13328
14	1986	40.2	3340	1	PCT-US06-33148-1645
15	1985.5	40.2	2804	1	PCT-US06-33148-1649
16	1964.5	39.8	3218	9	US-60-836-986-13329
17	1932.5	39.1	3195	6	US-10-276-115A-22
18	1927.5	39.0	4569	6	US-10-276-115A-3
19	1817	36.8	2663	1	PCT-US06-33148-1647
20	1472	29.8	2144	1	PCT-US06-33148-1643
21	1472	29.8	2209	1	PCT-US06-33148-1643
22	772	15.6	451	8	US-11-290-215A-174
23	455.5	9.2	731	8	US-11-433-832-31868
24	234	4.7	2350	8	US-11-433-832-31627
25	175	3.5	421	6	US-10-664-025A-2831
26	159	3.2	4997	9	US-60-836-986-2685
27	147	3.0	4128	1	PCT-US06-33712-1008
28	133.5	2.7	19341	9	US-60-836-986-206
29	133	2.7	5658	7	US-11-332-464-5
30	131.5	2.7	2808	6	US-10-587-052-3
31	131	2.7	4623	9	US-60-798-896-1
32	130.5	2.6	8192	1	PCT-US06-30281-11364
33	130	2.6	4578	6	US-10-669-920-757
34	130	2.6	339400	6	US-10-805-394A-1
35	129.5	2.6	3842	1	PCT-US06-20645-3
36	129.5	2.6	3846	8	US-11-433-832-47364
37	129.5	2.6	10011	1	PCT-US06-20645-1
38	129.5	2.6	10011	6	US-10-533-520-4370
39	129.5	2.6	10011	9	US-60-836-986-14427
40	129	2.6	1983043	6	US-10-961-644A-1
41	126.5	2.6	4778	8	US-11-437-729-4220
42	126.5	2.6	4793	7	US-11-520-715-26834
43	126.5	2.6	4816	8	US-11-437-729-4219
44	126.5	2.6	4816	8	US-11-475-062-8389
45	126.5	2.6	4828	6	US-10-533-520-6349

ALIGNMENTS

RESULT 1

US-10-550-797-1

; Sequence 1, Application US/10550797

; GENERAL INFORMATION:

; APPLICANT: Zehentner-Wilkinson, Barbara K.

; APPLICANT: Hayes, Dawn

; APPLICANT: Houghton, Raymond L.

; TITLE OF INVENTION: METHODS, COMPOSITIONS AND KITS FOR THE DETECTION

; TITLE OF INVENTION: AND MONITORING OF LUNG CANCER

; FILE REFERENCE: 210121.609USPC

; CURRENT APPLICATION NUMBER: US/10/550,797

; CURRENT FILING DATE: 2005-09-22

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: Corixa Invention Disclosure Database

; SEQ ID NO 1

; LENGTH: 3951

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-550-797-1

Alignment Scores:

Pred. No.: 0 Length: 3951

Score: 4942.00

Percent Similarity: 100.0%

Best Local Similarity: 100.0%

Query Match: 100.0%

DB: 6

Matches: 0

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

US-10-623-155-161 (1-943) x US-10-550-797-1 (1-3951)

QY

1 MetThrGlnArgSerIleAlaClyProIleCysAsnLeuLysPheValThrIleuVal 20

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QM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 13, 2006, 17:56:17 ; Search time 53208 Seconds  
(without alignments)  
1554.082 Million cell updates/sec

Title: US-10-623-155-161  
Perfect score: 4942  
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Scoring table: BLOSUM62  
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Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 86534536 seqs, 29229259966 residues

Total number of hits satisfying chosen parameters: 173069072

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	ID	Description
1	4942	100.0	3951 1	PCT-US01-47576-160 Sequence 160, App
2	4942	100.0	3951 3	PCT-US04-07451-1 Sequence 1, Appli
3	4942	100.0	3951 3	PCT-US04-23085-160 Sequence 160, App
4	4942	100.0	3951 24	US-Q9-510-376A-160 Sequence 160, App

5	4942	100.0	3951	28	US-09-662-786-160	Sequence 160, App
6	4942	100.0	3951	28	US-09-685-696-160	Sequence 160, App
7	4942	100.0	3951	30	US-09-735-705-160	Sequence 160, App
8	4942	100.0	3951	32	US-09-850-716-160	Sequence 160, App
9	4942	100.0	3951	32	US-09-850-716-160	Sequence 160, App
10	4942	100.0	3951	33	US-09-897-778-160	Sequence 160, App
11	4942	100.0	3951	41	US-10-117-983-160	Sequence 160, App
12	4942	100.0	3951	48	US-10-313-986-160	Sequence 160, App
13	4942	100.0	3951	52	US-10-623-155-160	Sequence 160, App
14	4942	100.0	3951	60	US-10-775-972-160	Sequence 160, App
15	4942	100.0	3951	62	US-10-922-124-160	Sequence 160, App
16	4942	100.0	3951	74	US-11-392-479-1	Sequence 1, Appl
17	4939	99.9	2832	1	PCT-US03-01450-30	Sequence 30, Appl
18	4939	99.9	2832	49	US-10-345-680-30	Sequence 30, Appl
19	4939	99.9	2832	73	US-11-302-678-30	Sequence 28, Appl
20	4939	99.9	2970	1	PCT-US03-01450-28	Sequence 28, Appl
21	4939	99.9	2970	49	US-10-345-680-28	Sequence 31, Appl
22	4939	99.9	2970	60	US-10-779-949-31	Sequence 28, Appl
23	4939	99.9	2970	73	US-11-302-678-28	Sequence 1, Appl
24	4939	99.9	2970	82	US-60-414-262-1	Sequence 615, App
25	4939	99.9	3669	51	US-10-529-348-615	Sequence 70, Appl
26	4939	99.9	3669	61	US-10-821-801-70	Sequence 196, App
27	4939	99.9	3671	1	PCT-US02-21338A-196	Sequence 518, App
28	4939	99.9	3671	1	PCT-US02-21338A-196	Sequence 196, App
29	4939	99.9	3671	41	US-10-126-052A-518	Sequence 196, App
30	4939	99.9	3671	41	US-10-188-832-196	Sequence 196, App
31	4939	99.9	3671	43	US-10-295-027-317	Sequence 317, App
32	4939	99.9	3671	43	US-10-295-027-1025	Sequence 1025, App
33	4939	99.9	3671	43	US-10-952-698-196	Sequence 196, App
34	4939	99.9	3955	85	US-60-679-970-1190	Sequence 1190, App
35	4939	99.9	4007	74	US-11-363-149-13	Sequence 13, Appl
36	4939	99.9	4007	74	US-11-363-151-13	Sequence 13, Appl
37	4939	99.9	4007	85	US-60-679-970-1191	Sequence 1191, App
38	4939	99.9	4007	86	US-60-710-726-53	Sequence 53, Appl
39	4939	99.9	4077	26	US-09-580-339B-1	Sequence 1, Appl
40	4939	99.9	4103	26	US-09-572-411-7294	Sequence 7294, App
41	4935	99.9	3671	41	US-10-126-052A-7	Sequence 7, Appl
42	4930	99.8	3604	42	US-10-240-425-360	Sequence 360, App
43	4930	99.8	3604	53	US-10-643-795A-13	Sequence 13, Appl
44	4930	99.8	3604	63	US-10-948-518-13	Sequence 13, Appl
45	4921	99.6	3190	3	PCT-US99-04703-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1	
PCT-US01-47576-160	
Sequence 160, Application PC/TUS0147576	
GENERAL INFORMATION:	
APPLICANT: Corixa Corporation	
APPLICANT: Wang, Tongcong	
APPLICANT: Wang, Aijun	
APPLICANT: Skeiky, Yasir A.W.	
APPLICANT: Li, Samuel X.	
APPLICANT: Kalos, Michael D.	
APPLICANT: Henderson, Robert A.	
APPLICANT: McNeill, Patricia D.	
APPLICANT: Fanger, Neil	
APPLICANT: Retter, Marc W.	
APPLICANT: Durham, Margarita	
APPLICANT: Fanger, Gary R.	
APPLICANT: Vedrick, Thomas S.	
APPLICANT: Carter, Darrick	
APPLICANT: Watanabe, Yoshihiro	
APPLICANT: Peckman, David W.	
APPLICANT: Cai, Feng	
APPLICANT: Fov, Teresa M.	
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY	
AND DIAGNOSIS OF LUNG CANCER	
FILE REFERENCE: 210121.45503PC	
CURRENT APPLICATION NUMBER: PCT/US01/47576	
DATE: 2001-11-30	

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DB	137	GCCTTAAGTTCAGAACTCCCATTCCTGGAGCTGGAGTACAGCTTCAAGACAAATGGGTAT	196
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DB	197	AATGATTTGCTCATTCGCAATTAATCCTCAGGTACCTGAGATCAGAACCTCATCTCAAA	256
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QY	181	LysProPheTyrIleAsnGlyGlnAsnGlnIleLysValThrArgCysSerSerAspIle	200
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GenCore version 5.1.9  
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OM protein - nucleic search, using frame\_plus\_p2n model

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5635.293 Million cell updates/sec

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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#### SUMMARIES

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2	4939	99.9	2970	8	US-11-302-678-28 Sequence 28, Appl
3	4939	99.9	4007	7	US-11-363-149-13 Sequence 13, Appl
4	4939	99.9	4007	7	US-11-363-151-13 Sequence 13, Appl
5	4388	88.8	2527	8	US-11-266-748A-184797 Sequence 184797,
6	1993	40.3	3311	6	US-10-700-439-87 Sequence 87, Appl
7	1965.5	39.8	3265	6	US-10-196-749-257 Sequence 257, Appl

8	1965.5	39.8	3265	8	US-11-101-316-69	Sequence 69, Appl
9	1965.5	39.8	3265	9	US-11-376-673-69	Sequence 69, Appl
10	1964.5	39.8	3204	8	US-11-302-678-31	Sequence 31, Appl
11	1964.5	39.8	3218	6	US-10-700-439-53	Sequence 53, Appl
12	1964.5	39.8	3218	8	US-11-266-748A-57517	Sequence 57517, A
13	1949.5	39.4	2754	8	US-11-302-678-33	Sequence 33, Appl
14	1880	38.0	1159	8	US-11-266-748A-184799	Sequence 184799,
15	1880	38.0	1159	8	US-11-266-748A-192237	Sequence 192237,
16	1403	28.4	1799	8	US-11-266-748A-184798	Sequence 184798,
17	1403	28.4	1799	8	US-11-266-748A-192296	Sequence 192296,
18	1040.5	21.1	1706	8	US-11-266-748A-4307	Sequence 4307, Ap
19	512.5	10.4	715	8	US-11-266-748A-5233	Sequence 5233, Ap
20	470	9.5	653	7	US-11-374-388-1851	Sequence 1851, Ap
21	468.5	9.5	533	7	US-11-374-388-1883	Sequence 1883, Ap
22	443.5	9.0	1000	8	US-11-266-748A-284991	Sequence 284991,
23	443.5	9.0	1000	8	US-11-266-748A-336420	Sequence 336420,
24	443.5	9.0	1000	8	US-11-266-748A-395149	Sequence 395149,
25	443.5	9.0	1000	8	US-11-266-748A-466195	Sequence 466195,
26	418	8.5	366	6	US-10-488-619-2714	Sequence 2714, Ap
27	357	7.2	1000	8	US-11-266-748A-222051	Sequence 222051,
28	357	7.2	1000	8	US-11-266-748A-287801	Sequence 287801,
29	357	7.2	1000	8	US-11-266-748A-339230	Sequence 339230,
30	357	7.2	1000	8	US-11-266-748A-398572	Sequence 398572,
31	357	7.2	1000	8	US-11-266-748A-469618	Sequence 469618,
32	327.5	6.6	833	8	US-11-266-748A-249419	Sequence 249419,
33	323.5	6.5	598	8	US-11-266-748A-5132	Sequence 5132, Ap
34	323.5	6.5	598	8	US-11-266-748A-63371	Sequence 63371, A
35	323.5	6.5	598	8	US-11-266-748A-66203	Sequence 66203, A
36	204	4.1	1000	8	US-11-266-748A-286631	Sequence 286631,
37	204	4.1	1000	8	US-11-266-748A-338060	Sequence 338060,
38	204	4.1	1000	8	US-11-266-748A-397144	Sequence 397144,
39	204	4.1	1000	8	US-11-266-748A-468190	Sequence 468190,
40	161.5	3.3	280	7	US-11-374-388-1868	Sequence 1868, Ap
41	154.5	3.1	432	7	US-11-190-172-2789	Sequence 2789, Ap
42	143.5	2.9	11784	8	US-11-266-748A-56711	Sequence 56711, A
43	134	2.7	3747	9	US-11-056-355B-91162	Sequence 91162, A
44	134	2.7	3747	9	US-11-056-355B-94918	Sequence 94918, A
45	130	2.6	4578	6	US-10-669-920-757	Sequence 757, App

#### ALIGNMENTS

#### RESULT 1

US-11-302-678-30  
; Sequence 30, Application US/11302678  
; Publication No. US2006008881A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: Silos-Santiago, Immaculada  
; APPLICANT: Venkateswarlu, Karicheti  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING  
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,  
; TITLE OF INVENTION: 641 260, 55089, 21407, 42032, 46556, 62553, 302, 323,  
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2058 OR 6351 MOLECULES.  
; FILE REFERENCE: MPI02-012PIRNM,OMNI  
; CURRENT APPLICATION NUMBER: US/11/302.678  
; CURRENT FILING DATE: 2005-12-14  
; PRIOR APPLICATION NUMBER: US/10/345,680  
; PRIOR FILING DATE: 2003-01-16  
; PRIOR APPLICATION NUMBER: US 60/349,511  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: US 60/360,500  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 60/365,041  
; PRIOR FILING DATE: 2002-03-15  
; PRIOR APPLICATION NUMBER: US 60/374,063  
; PRIOR FILING DATE: 2002-04-19  
; PRIOR APPLICATION NUMBER: US 60/403,468  
; PRIOR FILING DATE: 2002-08-14  
; PRIOR APPLICATION NUMBER: US 60/414,262  
; PRIOR FILING DATE: 2002-09-27  
; PRIOR APPLICATION NUMBER: US 60/419,986  
; PRIOR FILING DATE: 2002-10-21

GenCore version 5.1.9  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 13, 2006, 18:21:41 ; Search time 2578 Seconds

(without alignments)  
6741.994 Million cell updates/sec

Title: US-10-623-155-161

Perfect score: 4942

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Scoring table:

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Searched: 18992170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4942	100.0	3951	3	US-09-735-705-160

2	4942	100.0	3951	3	US-09-850-716A-160	Sequence 160, App
3	4942	100.0	3951	3	US-09-897-778-160	Sequence 160, App
4	4942	100.0	3951	3	US-09-466-396A-160	Sequence 160, App
5	4942	100.0	3951	6	US-10-007-700-160	Sequence 160, App
6	4942	100.0	3951	7	US-10-117-982-160	Sequence 160, App
7	4942	100.0	3951	9	US-10-313-985-160	Sequence 160, App
8	4942	100.0	3951	9	US-10-775-972-160	Sequence 160, App
9	4942	100.0	3951	10	US-10-922-124-160	Sequence 160, App
10	4942	100.0	3951	10	US-10-623-155-160	Sequence 160, App
11	4939	99.9	2832	7	US-10-345-680-30	Sequence 30, Appl
12	4939	99.9	2970	6	US-10-055-412B-31	Sequence 31, Appl
13	4939	99.9	2970	9	US-10-345-680-28	Sequence 28, Appl
14	4939	99.9	2970	9	US-10-779-949-31	Sequence 31, Appl
15	4939	99.9	3671	7	US-10-293-027-317	Sequence 317, App
16	4939	99.9	3671	7	US-10-295-027-1025	Sequence 1025, App
17	4939	99.9	3671	8	US-10-188-832-196	Sequence 196, App
18	4930	99.8	3604	8	US-10-240-425-360	Sequence 360, App
19	4930	99.8	3604	9	US-10-643-795A-13	Sequence 13, Appl
20	4930	99.8	3604	10	US-10-948-518-13	Sequence 13, Appl
21	4921	99.6	3190	6	US-10-270-595-3	Sequence 3, Appl
22	4921	99.6	3190	9	US-10-772-437-3	Sequence 3, Appl
23	4898.5	99.1	3156	3	US-09-919-172-86	Sequence 86, Appl
24	4898.5	99.1	3156	3	US-09-974-298-70	Sequence 70, Appl
25	4898.5	99.1	3156	9	US-10-752-986-86	Sequence 86, Appl
26	4790	96.9	2773	3	US-09-735-705-358	Sequence 358, App
27	4790	96.9	2773	3	US-09-850-716A-358	Sequence 358, App
28	4790	96.9	2773	3	US-09-897-778-358	Sequence 358, App
29	4790	96.9	2773	6	US-10-007-700-358	Sequence 358, App
30	4790	96.9	2773	7	US-10-117-982-358	Sequence 358, App
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36	4790	96.9	8031	3	US-09-850-716A-254	Sequence 254, App
37	4790	96.9	8031	3	US-09-897-778-254	Sequence 254, App
38	4790	96.9	8031	6	US-10-007-700-254	Sequence 254, App
39	4790	96.9	8031	7	US-10-117-982-254	Sequence 254, App
40	4790	96.9	8031	7	US-10-313-986-254	Sequence 254, App
41	4790	96.9	8031	9	US-10-775-972-254	Sequence 254, App
42	4790	96.9	8031	10	US-10-922-124-254	Sequence 254, App
43	4790	96.9	8031	10	US-10-623-155-254	Sequence 254, App
44	4707.5	95.3	2784	3	US-09-735-705-168	Sequence 168, App
45	4707.5	95.3	2784	3	US-09-850-716A-168	Sequence 168, App

#### ALIGNMENTS

#### RESULT 1

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US-09-735-705-160
; Sequence 160, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 160
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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Run on: October 13, 2006, 17:22:53 ; Search time 411 Seconds

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Title: US-10-623-155-161

Perfect score: 4942

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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delpop 6.0, Delcxt 7.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	4942	100.0	3951	3	US-09-480-884A-160
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6	4942	100.0	3951	3	US-09-466-396A-160
7	4942	100.0	3951	3	US-09-476-496A-160
8	4942	100.0	3951	3	US-09-630-940B-160

9	4942	100.0	3951	3	US-09-285-479-160	Sequence 160, App
10	4942	100.0	3951	3	US-10-007-700-160	Sequence 160, App
11	4939	99.9	2970	3	US-09-193-562B-31	Sequence 31, Appl
12	4939	99.9	2970	3	US-10-055-412B-31	Sequence 31, Appl
13	4921	99.6	3190	3	US-09-623-624-3	Sequence 3, Appl
14	4921	99.6	3190	3	US-10-270-595-3	Sequence 3, Appl
15	4908	99.3	3669	3	US-09-949-016-2224	Sequence 2224, Ap
16	4908	99.1	3156	3	US-09-919-172-86	Sequence 86, Appl
17	4790	96.9	2773	3	US-09-643-597-358	Sequence 358, App
18	4790	96.9	2773	3	US-09-630-940B-358	Sequence 358, App
19	4790	96.9	2773	3	US-10-007-700-358	Sequence 358, App
20	4790	96.9	8031	3	US-09-643-597-254	Sequence 254, App
21	4790	96.9	8031	3	US-09-480-884A-254	Sequence 254, App
22	4790	96.9	8031	3	US-09-542-615A-254	Sequence 254, App
23	4790	96.9	8031	3	US-09-606-421B-254	Sequence 254, App
24	4790	96.9	8031	3	US-09-476-496A-254	Sequence 254, App
25	4790	96.9	8031	3	US-09-630-940B-254	Sequence 254, App
26	4790	96.9	8031	3	US-10-007-700-254	Sequence 254, App
27	4707.5	95.3	2784	3	US-09-643-597-168	Sequence 168, App
28	4707.5	95.3	2784	3	US-09-480-884A-168	Sequence 168, App
29	4707.5	95.3	2784	3	US-09-542-615A-168	Sequence 168, App
30	4707.5	95.3	2784	3	US-09-606-421B-168	Sequence 168, App
31	4707.5	95.3	2784	3	US-09-476-496A-168	Sequence 168, App
32	4707.5	95.3	2784	3	US-09-630-940B-168	Sequence 168, App
33	4707.5	95.3	2784	3	US-09-285-479-168	Sequence 168, App
34	4707.5	95.3	2784	3	US-10-007-700-168	Sequence 168, App
35	4707.5	95.3	2784	3	US-09-643-597-167	Sequence 167, App
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38	3869	78.3	3362	3	US-09-480-884A-167	Sequence 167, App
39	3869	78.3	3362	3	US-09-542-615A-167	Sequence 167, App
40	3869	78.3	3362	3	US-09-606-421B-167	Sequence 167, App
41	3869	78.3	3362	3	US-09-476-496A-167	Sequence 167, App
42	3869	78.3	3362	3	US-09-630-940B-167	Sequence 167, App
43	3869	78.3	3362	3	US-09-285-479-167	Sequence 167, App
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45	3869	78.3	3362	3	US-09-643-597-160	Sequence 160, App

#### ALIGNMENTS

RESULT 1  
US-09-643-597-160  
; Sequence 160, Application US/09643597  
; Patent No. 6426072

GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun

; APPLICANT: Kalos, Michael D.

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Hosken, Nancy

; APPLICANT: Fanger, Gary R.

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Henderson, Robert A.

; APPLICANT: McNeill, Patricia D.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 210121.455C11

; CURRENT APPLICATION NUMBER: US/09/643,597

; CURRENT FILING DATE: 2000-08-21

; NUMBER OF SEQ ID NOS: 369

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 160

; LENGTH: 3951

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-643-597-160

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Score: 4942.00

Length: 3951

Matches: 943

GenCore version 5.1.9  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	ID	Description
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5	3861	97.7	PCT-US06-33148-1637	Sequence 1637, Appl
6	3861	97.7	US-11-431-708-4126	Sequence 4126, Appl
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9	2827.8	71.6	US-11-371-354-64288	Sequence 64288, A
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14	552.2	14.0	US-11-475-062-9462	Sequence 9462, Appl
15	550.6	13.9	PCT-US06-33148-1649	Sequence 1649, Appl
16	550.6	13.9	PCT-US06-33148-23	Sequence 23, Appl
17	550.6	13.9	US-11-475-062-9463	Sequence 9463, Appl
18	550.6	13.9	US-60-836-986-13328	Sequence 13328, A
19	550.6	13.9	PCT-US06-33148-1645	Sequence 1645, Appl
20	494.2	12.5	US-11-290-215A-172	Sequence 172, Appl
21	462.4	11.7	PCT-US06-33148-1647	Sequence 1647, Appl
22	449.4	11.4	US-11-290-215A-174	Sequence 174, Appl
23	448.8	11.4	US-11-290-215A-370	Sequence 370, Appl
24	434	11.0	US-10-276-115A-3	Sequence 3, Appl

## ALIGNMENTS

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; Sequence 1, Application US/10550797  
; GENERAL INFORMATION:  
; APPLICANT: Zehntner-Wilkinson, Barbara K.  
; APPLICANT: Hayes, Dawn  
; APPLICANT: Houghton, Raymond L.  
; TITLE OF INVENTION: METHODS, COMPOSITIONS AND KITS FOR THE DETECTION  
; FILE REFERENCE: 210121.60USPC  
; CURRENT APPLICATION NUMBER: US/10/550,797  
; CURRENT FILING DATE: 2005-09-22  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: Corixa Invention Disclosure Database  
; SEQ ID NO 1  
; LENGTH: 3951  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-550-797-1

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DB	121	TGTGACTCTCTGGTGTCTTAAGTTTCAAGTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCT	180		
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26	168.2	4.3	173	8	US-11-290-215A-173	Sequence 173, App
27	123.2	3.1	2350	8	US-11-433-832-31627	Sequence 31627, A
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30	3613.2	91.5	3669	61	US-10-529-348-615	Sequence 615, App
31	3613.2	91.5	3669	61	US-10-821-801-70	Sequence 70, Appl
32	3578.8	90.6	4077	26	US-09-580-339B-1	Sequence 1, Appli
33	3547.2	89.8	3671	1	PCT-US02-21338-156	Sequence 196, App
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38	3547.2	89.8	3671	43	US-10-295-027-1025	Sequence 1025, Ap
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41	3507	88.8	3604	42	US-10-240-425-360	Sequence 360, App
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ALIGNMENTS

RESULT 1

PCT-US01-47576-160

Sequence 160, Application PC/TUS0147576

GENERAL INFORMATION:

APPLICANT: Corixa Corporation

APPLICANT: Wang, Tongtong

APPLICANT: Wang, Aijun

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Li, Samuel X.

APPLICANT: Kalos, Michael D.

APPLICANT: Henderson, Robert A.

APPLICANT: McNeill, Patricia D.

APPLICANT: Fanger, Neil

APPLICANT: Retter, Marc W.

APPLICANT: Durham, Margarita

APPLICANT: Fanger, Gary R.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Carter, Darrick

APPLICANT: Watanabe, Yoshihiro

APPLICANT: Peckman, David W.

APPLICANT: Cai, Feng

APPLICANT: Foy, Teresa M.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.45503PC

CURRENT APPLICATION NUMBER: PCT/US01/47576

CURRENT FILING DATE: 2001-11-30

NUMBER OF SEQ ID NOS: 469

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 160

LENGTH: 3951

TYPE: DNA

ORGANISM: Homo sapiens

PCT-US01-47576-160

Query Match 100.0%; Score 3951; DB 1; Length 3951;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3951; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 TCTGCATCCATATTGAAACCTGACACAAATGTATGACAGCGCTCAGTGTGAGTGAACCTG 60

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1	3939.8	99.7	4007	7	US-11-363-149-13	Sequence 13, Appl	
2	3939.8	99.7	4007	7	US-11-363-151-13	Sequence 13, Appl	
3	2930	74.2	2970	8	US-11-302-678-28	Sequence 28, Appl	
4	2827.2	71.6	2832	8	US-11-302-678-30	Sequence 30, Appl	
5	2497.4	63.2	2527	8	US-11-266-748A-184797	Sequence 184797,	
6	1748.6	44.3	1799	8	US-11-266-748A-184798	Sequence 184798	
7	1748.6	44.3	1799	8	US-11-266-748A-192296	Sequence 192296,	
8	1138	28.8	1159	8	US-11-266-748A-184799	Sequence 184799,	
9	1138	28.8	1159	8	US-11-266-748A-192297	Sequence 192297,	
10	966	24.4	1000	8	US-11-266-748A-116637	Sequence 116637,	
11	966	24.4	1000	8	US-11-266-748A-158801	Sequence 158801,	
12	966	24.4	1000	8	US-11-266-748A-398053	Sequence 398053,	
13	966	24.4	1000	8	US-11-266-748A-469099	Sequence 469099,	
14	652.8	16.5	3204	8	US-11-302-678-31	Sequence 31, Appl	
15	652.8	16.5	3218	6	US-10-700-439-53	Sequence 53, Appl	
16	652.8	16.5	3218	8	US-11-266-748A-57517	Sequence 57517, A	
17	646.8	16.4	3265	6	US-10-196-749-257	Sequence 257, App	
18	646.8	16.4	3265	8	US-11-101-316-69	Sequence 69, Appl	
19	646.8	16.4	3265	9	US-11-376-673-69	Sequence 69, Appl	
20	645.4	16.3	3254	8	US-11-302-678-31	Sequence 31, Appl	
21	550.6	13.9	3311	6	US-10-700-439-87	Sequence 87, Appl	
22	533.8	13.5	538	8	US-11-266-748A-82206	Sequence 82206, A	
23	533.8	13.5	538	8	US-11-266-748A-135017	Sequence 135017,	

GenCore version 5.1.9  
 Copyright (c) 1993 - 2006 Bioceleration Ltd.  
 OM nucleic - nucleic search, using sw model  
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 (without alignments)  
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Title: US-10-623-155-160  
 Perfect score: 3951  
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Scoring table: IDENTITY NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Published Applications NA Main:  
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 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq.\*  
 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq.\*  
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 13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq.\*  
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 16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	3951	100.0	3951	3	US-09-850-716A-160
3	3951	100.0	3951	3	US-09-897-778-160
4	3951	100.0	3951	3	US-09-466-396A-160
5	3951	100.0	3951	6	US-10-007-700-160
6	3951	100.0	3951	7	US-10-117-982-160
7	3951	100.0	3951	7	US-10-313-986-160
8	3951	100.0	3951	9	US-10-775-972-160
9	3951	100.0	3951	10	US-10-923-124-160
10	3951	100.0	3951	10	US-10-623-155-160
11	3547.2	89.8	3671	7	US-10-295-027-317
12	3547.2	89.8	3671	7	US-10-295-027-1025
13	3547.2	89.8	3671	8	US-10-188-832-136
14	3507	88.8	3604	8	US-10-240-425-360
15	3507	88.8	3604	9	US-10-643-795A-13
16	3507	88.8	3604	10	US-10-948-518-13
17	3104.4	78.6	3156	3	US-09-919-172-86

18	3104.4	78.6	3156	3	US-09-974-298-70
19	3104.4	78.6	3156	9	US-10-752-986-86
20	3101.2	78.5	3190	6	US-10-270-595-3
21	3101.2	78.5	3190	9	US-10-772-437-3
22	2930	74.2	2970	6	US-10-055-412B-31
23	2930	74.2	2970	7	US-10-345-680-28
24	2930	74.2	2970	7	US-10-779-949-31
25	2827.2	71.6	2832	7	US-10-345-680-30
26	2800.8	70.9	3362	3	US-09-735-705-167
27	2800.8	70.9	3362	3	US-09-850-716A-167
28	2800.8	70.9	3362	3	US-09-897-778-167
29	2800.8	70.9	3362	3	US-09-466-396A-167
30	2800.8	70.9	3362	6	US-10-007-700-167
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34	2800.8	70.9	3362	10	US-10-923-124-167
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45	2772	70.2	2784	10	US-10-623-155-168

ALIGNMENTS

RESULT 1  
 ; Sequence 160, Application US/09735705  
 ; Patent No. US20020052329A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, Tongtong  
 ; APPLICANT: Fan, Liqun  
 ; APPLICANT: Kalos, Michael D.  
 ; APPLICANT: Bangur, Chaitanya S.  
 ; APPLICANT: Hosken, Nancy  
 ; APPLICANT: Ranger, Gary R.  
 ; APPLICANT: Li, Samuel X.  
 ; APPLICANT: Wang, Aijun  
 ; APPLICANT: Skeiky, Yasir A.W.  
 ; APPLICANT: Henderson, Robert A.  
 ; APPLICANT: McNeill, Patricia D.  
 ; APPLICANT: Ranger, Neil  
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
 ; FILE REFERENCE: 210121.455C14  
 ; CURRENT APPLICATION NUMBER: US/09/735, 705  
 ; CURRENT FILING DATE: 2000-12-12  
 ; NUMBER OF SEQ ID NOS: 419  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 160  
 ; LENGTH: 3951  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapien  
 ; US-09-735-705-160

Query Match 100.0%; Score 3951; DB 3; Length 3951;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 3951; Conservative 0; Mismatches 0; Gaps 0;

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